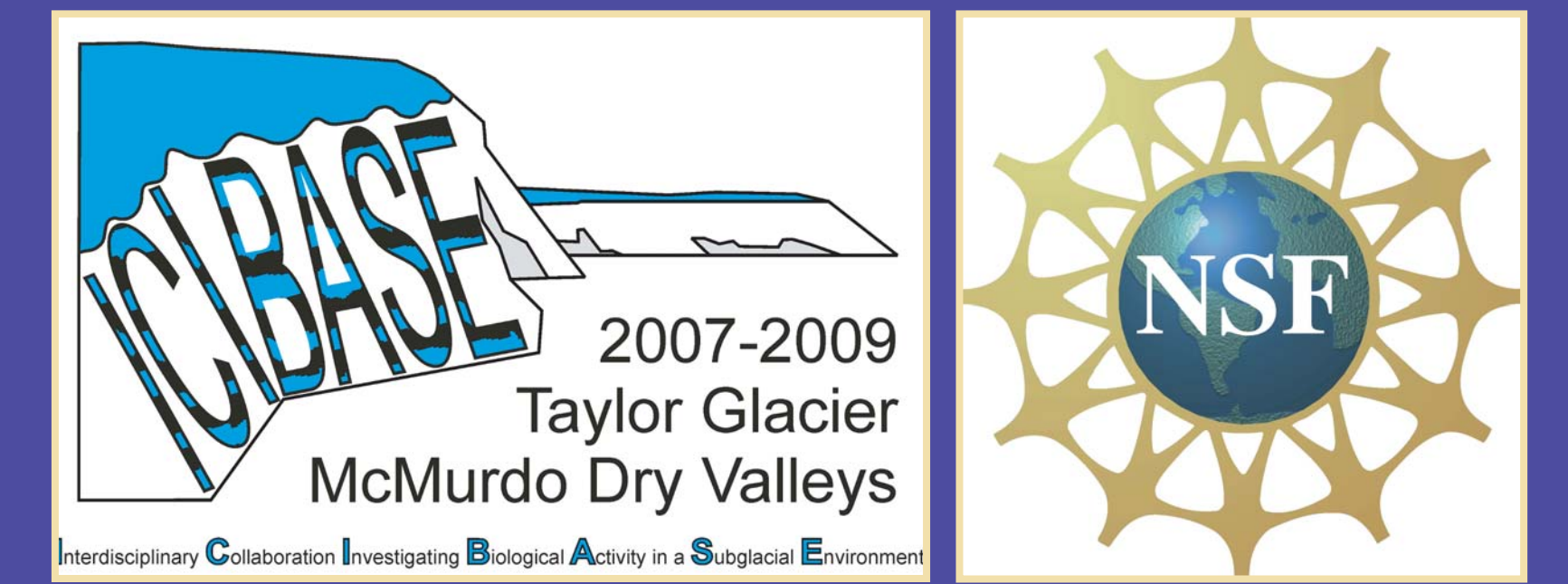


Geomicrobiology of Sediment-rich Basal Ice from Taylor Glacier

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I. Scientific Problem:

Are microorganisms in sediment-rich ice from the basal ice zone of Taylor Glacier metabolically active?

II. Background:

Gas measurements from ice samples from a basal ice profile collected in 1999 suggest heterotrophic microbial activity (Figure 1a). Selected basal ice samples from the profile, were melted and incubated at 2°C, demonstrating heterotrophic activity (Figure 1b).

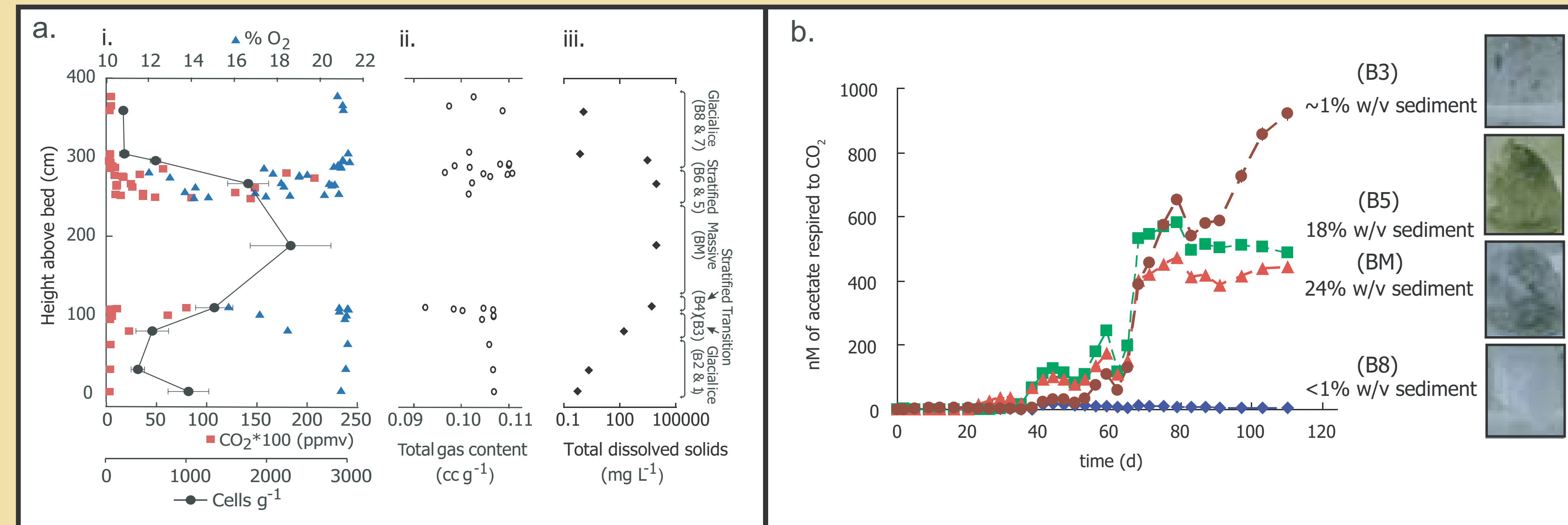


Figure 1. a. Vertical profile of Taylor Glacier basal ice showing the concentration of (i) bacterial cells ($\pm$ one standard deviation), CO₂ and O₂, (ii) total gas content, and (iii) total dissolved solids. Brackets and text on right indicate basal ice stratigraphy and sample designations. Gas measurements are from Samyn et al., (2005). b. Heterotrophic microbial respiration at 2°C from melted Taylor Glacier ice samples, amended with 14C-acetate only. No additional nutrients were added. Chemical, cell and gas composition data for these samples is shown in a.

III. Field Site and Tunnel Construction at Taylor Glacier:



Figure 2. Location of Taylor Glacier, McMurdo Dry Valleys, Antarctica. Image from <http://huey.colorado.edu/77DegreesSouth/week1.html>

Photo: Taylor Glacier. Arrow denotes location of subglacial tunnel constructed at the north margin of the glacier.

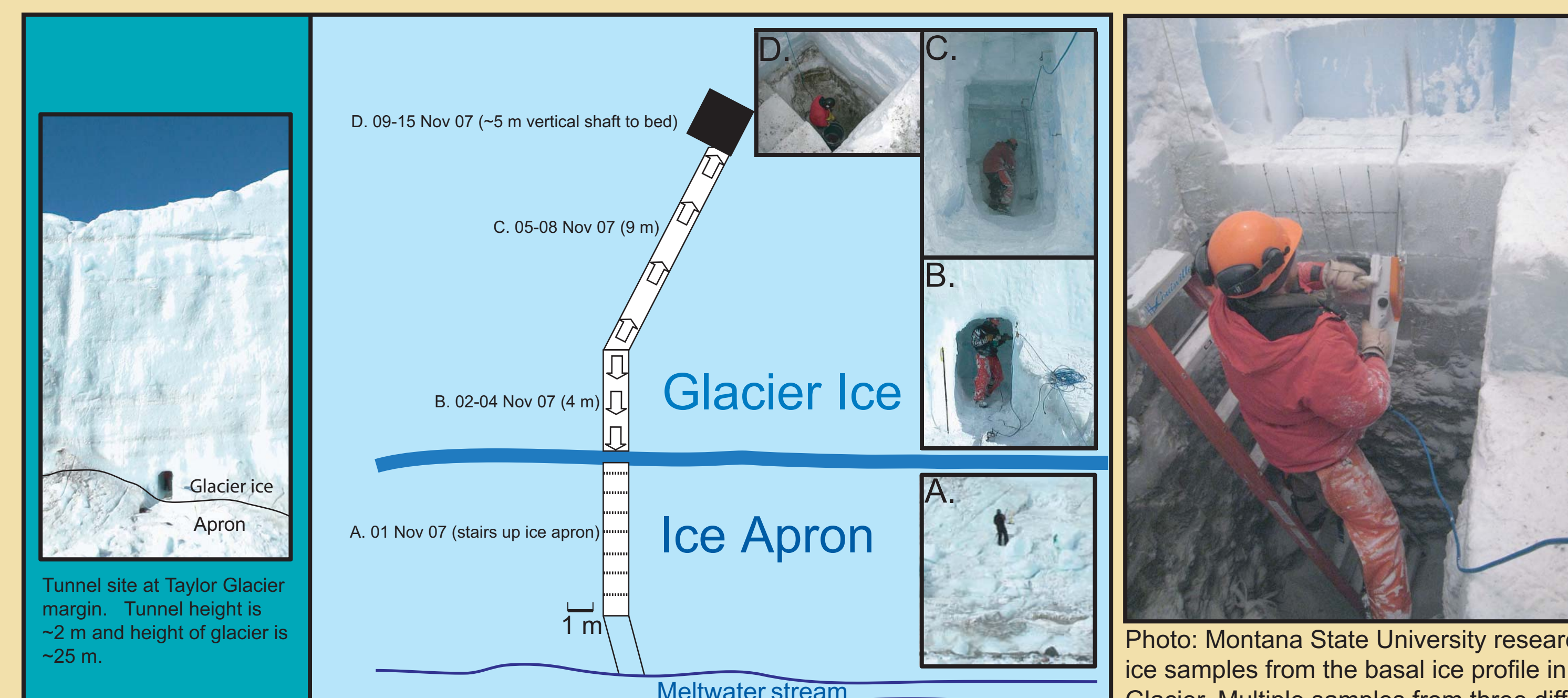


Photo: Montana State University researcher Tim Brox collects ice samples from the basal ice profile in the tunnel at Taylor Glacier. Multiple samples from three different ice zones were collected across a 400 cm vertical profile for microbiological and geochemical analyses.

IV. Stratigraphy of basal ice profile:

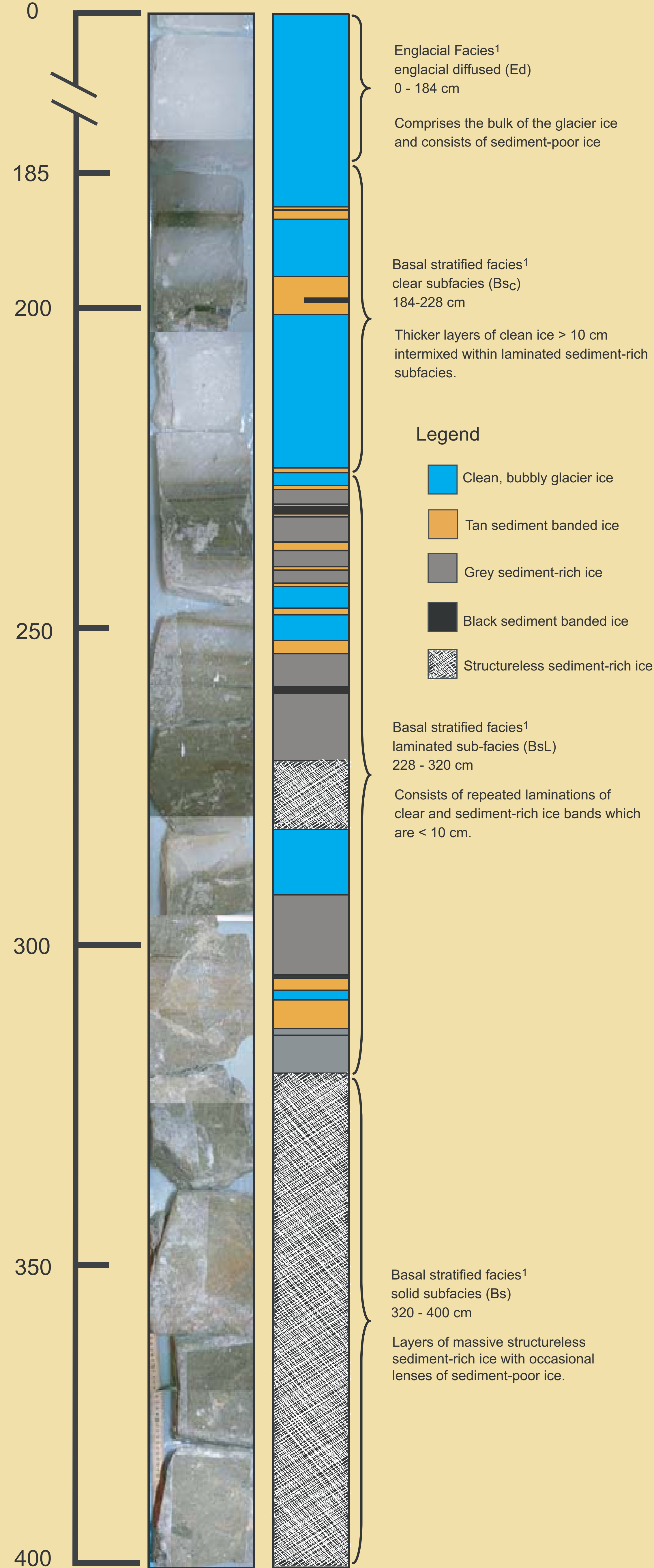
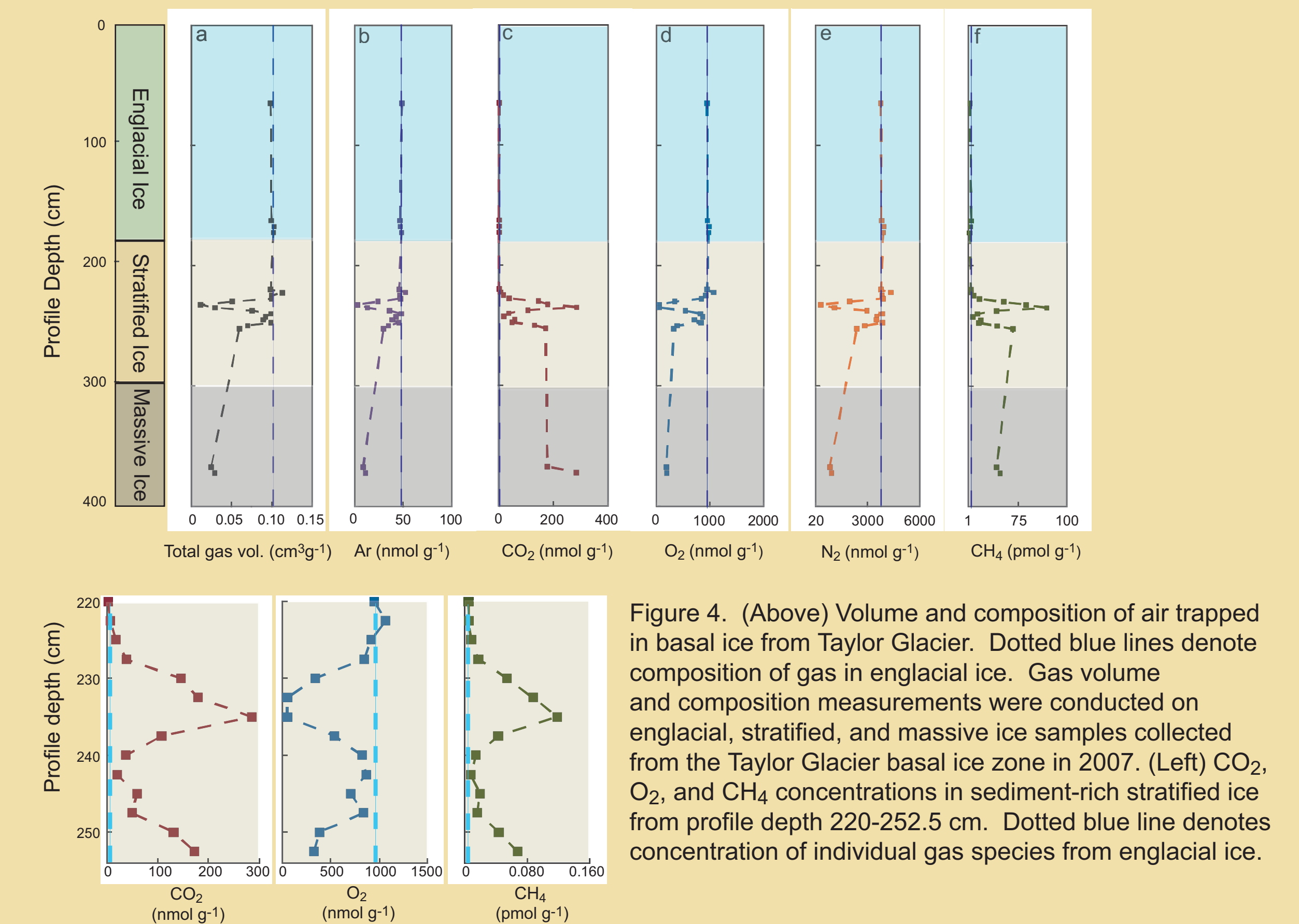


Figure 3. Stratigraphy of basal ice profile collected from TG. Depths are in cm and measured from the top of the basal ice profile collected.

¹Facies identification modified from Sharp et al., (1994)

V. Gas Chemistry:



VI. Aqueous Chemistry:

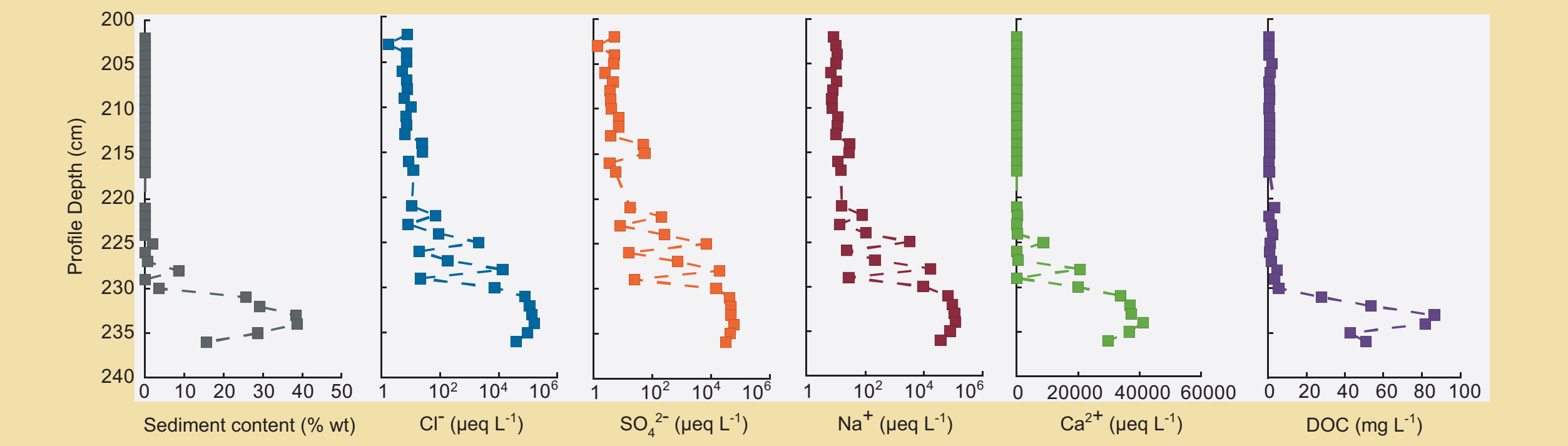


Figure 5. Sediment content and concentration of dissolved ions and dissolved organic carbon in melted basal ice from TG profile. Measurements were made at 1 cm vertical resolution across the basal ice profile from depths 201-236 cm.

VII. Microbial Community Composition:

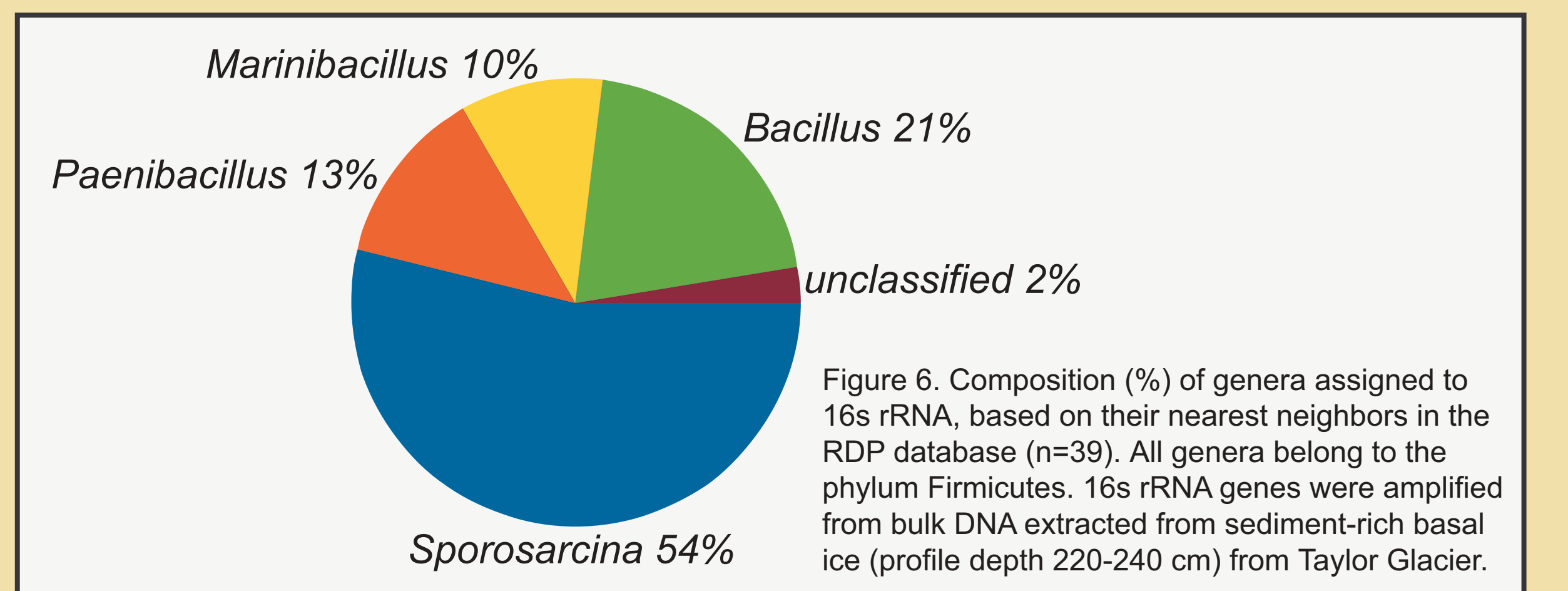


Figure 6. Composition (%) of genera assigned to 16s rRNA, based on their nearest neighbors in the RDP database (n=39). All genera belong to the phylum Firmicutes. 16s rRNA genes were amplified from bulk DNA extracted from sediment-rich basal ice (profile depth 220-240 cm) from Taylor Glacier.

VIII. Conclusions:

Sediment-rich basal ice contains heterotrophic microorganisms and a significant amount of dissolved organic carbon and other nutrients.

Microbial activity remains a plausible mechanism to explain gas (CO₂, O₂, and CH₄) anomalies in the sediment-rich ice.

The subglacial microbial community is dominated by members of the bacterial phylum *Firmicutes*.

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¹Sharp, M., Jouzel, J., Hubbard, B., Lawson, W., (1994) The character, structure, and origin of the basal ice layer of a surge-type glacier. *Journal of Glaciology*: 40, 327-340.

Samyn, D., Fitzsimons, S., Lorrain, R.D., (2005) Strain-induced phase changes within cold basal ice from Taylor Glacier, indicated by textural and gas analysis. *Journal of Glaciology*: 611-620